Draper
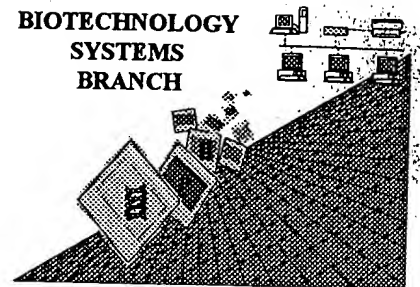
RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _08/383,676_

Art Unit / Team No. : _1646_

Date Processed by STIC: _3/22/99_

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED   CORRECTION**

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 _____ Wrong Designation

Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

> This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
 1                                         SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5    (i) APPLICANT: Hauptman, et al.
 6
 7    (ii) TITLE OF INVENTION: TNF RECEPTORS, TNF BINDINGBINDING PROTEINS, AND DNAs CODIN
 8
 9    (iii) NUMBER OF SEQUENCES 64
10
11    (iv) CORRESPONDENCE ADDRESS:
12    (A)ADDRESSEE:John J. McDonnell
13    (B)STREET:300 S. Wacker Drive
14    (C)CITY:Chicago
15    (D)STATE:IL
16    (E)COUNTRY:USA
17    (F)ZIP:60606
18
19    (v) COMPUTER READABLE FORM:
20    (A) MEDIUM TYPE: Floppy disk
21    (B) COMPUTER: IBM PC compatible
22    (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23    (D) SOFTWARE:ASCII
24
25    (vi) CURRENT APPLICATION DATA:
26    (A) APPLICATION NUMBER:08/464,312
27    (B) FILING DATE:June 7, 1995
28    (C) CLASSIFICATION:
29
30    (viii) ATTORNEY/AGENT INFORMATION:
31    (A) NAME:John J. McDonnell
32    (B) REGISTRATION NUMBER:  26,949
33    (C) REFERENCE/DOCKET NUMBER:98,385-A
34
35    (ix) TELECOMMUNICATION INFORMATION:
36    (A) TELEPHONE:312-913-0001
37    (B) TELEFAX:312-913-9808
38
```

Handwritten annotations: ? 72 shows (p.19) see item 3 on Erro Summary sheet

383,676

Suggestion: Consult Sequence Rules for valid format

ERRORED SEQUENCES FOLLOW:

```
39    (2) INFORMATION FOR SEQ ID NO:1:
```

```
40
41    (i) SEQUENCE CHARACTERISTICS:
-->   42    (A) LENGTH:1365 bases
43    (B) TYPE:nucleic acid
44    (C) STRANDEDNESS:single
45    (D) TOPOLOGY:linear
46
47    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
48
49    ATGGGCCTCT CCACCGTGCC TGACCTGCTG CTGCCACTGG TGCTCCTGGA    50   GCTGTTGGTG GGAATATACC
50
```

(handwritten: all text must be visible)

(handwritten: insert hard returns after each cumulative base total)

```
51    (2) INFORMATION FOR SEQ ID NO:2:
52
53    (i) SEQUENCE CHARACTERISTICS:
-->   54    (A) LENGTH:483 bases
55    (B) TYPE:nucleic acid
56    (C) STRANDEDNESS:single
57    (D) TOPOLOGY:linear
58
59    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
60
61    GATAGTGTGT GTCCCCAAGG AAAATATATC CACCCTCAAA ATAATTCGAT    50 TTGCTGTACC AAGTGCCACA A
62
```

(handwritten: same etc)

```
63    (2) INFORMATION FOR SEQ ID NO:3:
64
65    (i) SEQUENCE CHARACTERISTICS:
-->   66    (A) LENGTH:455 amino acids
-->   67    (B) TYPE:polypeptide
68
-->   69    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
70
71    Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
72                    5                   10                  15
73    Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
74                   20                   25                  30
75    Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
76                   35                   40                  45
77    Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
78                   50                   55                  60
79    Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
80                   65                   70                  75
81    Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
82                   80                   85                  90
83    Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
84                   95                  100                 105
85    Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
86                  110                  115                 120
87    Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
88                  125                  130                 135
89    Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
90                  140                  145                 150
```

(handwritten: the only valid response is "amino acid")

(handwritten: (D)TOPOLOGY: ← add this MANDATORY subheading and response for all sequence types. This is a global error in the amino acid sequence.)

INPUT SET: S31123.raw

```
 91   Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
 92               155             160             165
 93   Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
 94               170             175             180
 95   Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
 96               185             190             195
 97   Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
 98               200             205             210
 99   Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
100               215             220             225
101   Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
102               230             235             240
103   Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
104               245             250             255
105   Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
106               260             265             270
107   Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
108               275             280             285
109   Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
110               290             295             300
111   Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
112               305             310             315
113   Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
114               320             325             330
115   Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala
116               335             340             345
117   His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
118               350             355             360
119   Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val
120               365             370             375
121   Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu
122               380             385             390
123   Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala
124               395             400             405
125   Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu
126               410             415             420
127   Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu
128               425             430             435
129   Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala
130               440             445             450
131   Pro Ser Leu Leu Arg
132               455
133
```

```
134   (2) INFORMATION FOR SEQ ID NO:4:
135
136   (i) SEQUENCE CHARACTERISTICS:
137   (A) LENGTH:161 amino acids
138   (B) TYPE:polypeptide
139
140   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
141
142   Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
```

INPUT SET: S31123.raw

```
143                          5                    10                        15
144        Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn
145                         20                    25                        30
146        Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu
147                         35                    40                        45
148        Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu
149                         50                    55                        60
150        Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser
151                         65                    70                        75
152        Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
153                         80                    85                        90
154        Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn
155                         95                   100                       105
156        Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
157                        110                   115                       120
158        Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg
159                        125                   130                       135
160        Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu
161                        140                   145                       150
162        Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
163                        155                   160
164
```

```
165        (2) INFORMATION FOR SEQ ID NO:5:
166
167        (i) SEQUENCE CHARACTERISTICS:
-->  168        (A) LENGTH:157 bases
169        (B) TYPE:nucleic acid
170        (C) STRANDEDNESS:single
171        (D) TOPOLOGY:linear
172
173        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
174
175        CAGGGGAAA ATATTCACCC TCAAATAAT TCGATTTGCT GTACCAAGTG      50 CCACAAAGG AAACTACTTG TA
176
```

hard returns

```
177        (2) INFORMATION FOR SEQ ID NO:6:
178
179        (i) SEQUENCE CHARACTERISTICS:
-->  180        (A) LENGTH:13 amino acids
-->  181        (B) TYPE:polypeptide
182
-->  183        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
184
185        Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln
186                          5                   10
187
```

and add (D) TOPOLOGY: leading and response

```
188        (2) INFORMATION FOR SEQ ID NO:7:
189
190        (i) SEQUENCE CHARACTERISTICS:
-->  191        (A) LENGTH:11 amino acids
-->  192        (B) TYPE:polypeptide
```

same error

INPUT SET: S31123.raw

```
        193
-->     194   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
        195
        196   Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
        197                 5                  10
        198
```

```
        199   (2) INFORMATION FOR SEQ ID NO:8:
        200
        201   (i) SEQUENCE CHARACTERISTICS:
-->     202   (A) LENGTH:12 amino acids              same
-->     203   (B) TYPE:polypeptide)
        204
-->     205   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
        206
        207   Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys
        208                 5                  10
        209
```

```
        210   (2) INFORMATION FOR SEQ ID NO:9:
        211
        212   (i) SEQUENCE CHARACTERISTICS:
-->     213   (A) LENGTH:13 amino acids          same
-->     214   (B) TYPE:polypeptide )
        215
-->     216   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
        217
        218   Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys
        219                 5                  10
        220          (2) <— insert this number in all sequence — (2) remains the
        221   (11) INFORMATION FOR SEQ ID NO:10:                              same
        222
        223   (i) SEQUENCE CHARACTERISTICS:
-->     224   (A) LENGTH:14 amino acids
-->     225   (B) TYPE:polypeptide)
        226
-->     227   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
        228
        229   Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
        230                 5                  10
        231
```

```
-->     232   (2) INFORMATION FOR SEQ ID NO:11:
        233
        234   (i) SEQUENCE CHARACTERISTICS:
-->     235   (A) LENGTH:15 amino acids
-->     236   (B) TYPE:polypeptide )
        237
-->     238   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
        239
        240   Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg
        241                 5                  10                  15
        242
```

```
      243   (2) INFORMATION FOR SEQ ID NO:12:
      244
      245   (i) SEQUENCE CHARACTERISTICS:
-->   246   (A) LENGTH:13 amino acids
-->   247   (B) TYPE:polypeptide
      248
-->   249   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
      250
      251   Gly Thr Tyr Ley Tyr Asn Asp Cys Pro Gly Pro Gly Gln
      252                   5                   10
      253
```

```
      254   (2) INFORMATION FOR SEQ ID NO:13:
      255
      256   (i) SEQUENCE CHARACTERISTICS:
-->   257   (A) LENGTH:13 amino acids
-->   258   (B) TYPE:polypeptide
      259
-->   260   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
      261
      262   Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp
      263                   5                   10
      264
```

```
      265   (2) INFORMATION FOR SEQ ID NO:14:
      266
      267   (i) SEQUENCE CHARACTERISTICS:
-->   268   (A) LENGTH:20 amino acids
-->   269   (B) TYPE:polypeptide
      270
-->   271   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
      272
      273   Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg
      274                   5                   10                  15
      275   Asp Thr Val Cys Gly
      276                   20
      277
```

```
      278   (2) INFORMATION FOR SEQ ID NO:15:
      279
      280   (i) SEQUENCE CHARACTERISTICS:
-->   281   (A) LENGTH:19 amino acids
-->   282   (B) TYPE:polypeptide
      283
-->   284   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
      285
      286   Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His
      287                   5                   10                  15
      288   Lys Gly Xaa Tyr
      289
      290
```

```
      291   (2) INFORMATION FOR SEQ ID NO:16:
```

```
     292
     293   (i) SEQUENCE CHARACTERISTICS:
-->  294   (A) LENGTH:18 amino acids
-->  295   (B) TYPE:polypeptide
     296
-->  297   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
     298
     299   Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr
     300                       5                   10                  15
     301   Xaa Xaa Arg
     302
     303
```

```
     304   (2) INFORMATION FOR SEQ ID NO:17:
     305
     306   (i) SEQUENCE CHARACTERISTICS:
-->  307   (A) LENGTH:14 amino acids
-->  308   (B) TYPE:polypeptide
     309
-->  310   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
     311
     312   Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg
     313                       5                   10
     314
```

```
     315   (2) INFORMATION FOR SEQ ID NO:18:
     316
     317   (i) SEQUENCE CHARACTERISTICS:
-->  318   (A) LENGTH:14 amino acids
-->  319   (B) TYPE:polypeptide
     320
-->  321   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
     322
     323   Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
     324                       5                   10
     325
```

```
     326   (2) INFORMATION FOR SEQ ID NO:19:
     327
     328   (i) SEQUENCE CHARACTERISTICS:
-->  329   (A) LENGTH:13 amino acids
-->  330   (B) TYPE:polypeptide
     331
-->  332   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
     333
     334   Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln
     335                       5                   10
     336
```

```
     481   (2) INFORMATION FOR SEQ ID NO:32:
     482
     483   (i) SEQUENCE CHARACTERISTICS:
-->  484   (A) LENGTH:14 amino acids
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/383,676*

INPUT SET: S31123.raw

```
-->   485   (B) TYPE:polypeptide
      486
-->   487   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
      488
      489   Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
      490                     5                   10
      491
```

```
      492   (2) INFORMATION FOR SEQ ID NO:33:
      493
      494   (i) SEQUENCE CHARACTERISTICS:
-->   495   (A) LENGTH:14 amino acids
-->   496   (B) TYPE:polypeptide
      497
-->   498   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
      499
      500   Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys
      501                     5                   10
      502
```

```
      647   (2) INFORMATION FOR SEQ ID NO:46:
      648
      649   (i) SEQUENCE CHARACTERISTICS:
-->   650   (A) LENGTH:51 amino acids
-->   651   (B) TYPE:polypeptide
      652
-->   653   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
      654
      655   Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
      656                     5                   10                  15
      657   Lys Cys His Lys Gly Thr Tyr Ley Tyr Asn Asp Cys Pro Gly Pro
      658                     20                  25                  30
      659   Gly Gln Asp Thr Asp Cys Arg Gly Cys Glu Ser Gly Ser Phe Thr
      660                     35                  40                  45
      661   Ala Ser Glu Asn Asn Lys
      662                     50
      663
```

```
      664   (2) INFORMATION FOR SEQ ID NO:47:
      665
      666   (i) SEQUENCE CHARACTERISTICS:
-->   667   (A) LENGTH:158 bases
      668   (B) TYPE:nucleic acid
      669   (C) STRANDEDNESS:single
      670   (D) TOPOLOGY:linear
      671
      672   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
      673
      674   CAGGGGAAAT ATATTCACCC TCAAAATAAT TCGATTTCGT GTACCAAGTC   50 GCACAAAGGA ACCTACTTGT A
      675
```

```
      762   (2) INFORMATION FOR SEQ ID NO:55:
      763
```

```
       764   (i) SEQUENCE CHARACTERISTICS:
-->    765   (A) LENGTH:63 bases
       766   (B) TYPE:nucleic acid
       767   (C) STRANDEDNESS:single
       768   (D) TOPOLOGY:linear
       769
       770   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
       771
       772   AGCTCTAGAG ATTCGCGGCC GCTCGAGGTA CCGGATCCAT CGATGTCGAC    50 CTGCAGAAGC TTG
       773
```

```
       774   (2) INFORMATION FOR SEQ ID NO:56:
       775
       776   (i) SEQUENCE CHARACTERISTICS:
-->    777   (A) LENGTH:64 bases
       778   (B) TYPE:nucleic acid
       779   (C) STRANDEDNESS:single
       780   (D) TOPOLOGY:linear
       781
       782   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
       783
       784   CTAGCAAGCT TCTGCAGGTC GACATCGATG GATCCGGTAC CTCGAGCGGC    50 CGCGAATTCT CTAG
       785
```

```
       810   (2) INFORMATION FOR SEQ ID NO:59:
       811
       812   (i) SEQUENCE CHARACTERISTICS:
-->    813   (A) LENGTH:81 bases
       814   (B) TYPE:nucleic acid
       815   (C) STRANDEDNESS:single
       816   (D) TOPOLOGY:linear
       817
       818   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
       819
       820   CACAGTCGAC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT    50 CAAACAGACA CCATGGGCCT C
       821
```

```
       870   (2) INFORMATION FOR SEQ ID NO:64:
       871
       872   (i) SEQUENCE CHARACTERISTICS:
-->    873   (A) LENGTH:30 bases      18 shown
       874   (B) TYPE:nucleic acid
       875   (C) STRANDEDNESS:single
       876   (D) TOPOLOGY:linear
       877
       878   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
       879
       880   GTCCAATTAT GTCACACC                                       18
       881
```

```
       882   (2) INFORMATION FOR SEQ ID NO:65:
       883
       884   (i) SEQUENCE CHARACTERISTICS:
```

INPUT SET: S31123.raw

```
-->   885   (A) LENGTH:1334 bases
      886   (B) TYPE:nucleic acid
      887   (C) STRANDEDNESS:single
      888   (D) TOPOLOGY:linear
      889
      890   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
      891
      892   GAATTCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC      50  TGGGACCAGG CCGTGAT
      893
-->   894   TAGCTGTCTG GC                                             212
      895
      896   ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG TTC   257
      897   Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
      898                       5                   10                  15
      899
      900   CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG   302
      901   Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
      902                       20                  25                  30
      903
      904   GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC   347
      905   Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
      906                       35                  40                  45
      907
      908   CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC   392
      909   Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
      910                       50                  55                  60
      911
      912   AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG   437
      913   Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
      914                       65                  70                  75
      915
      916   GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC   482
      917   Gly Gln Asp The Asp Cys Arg Glu Cys Gly Ser Gly Ser Phe Thr
      918                       80                  85                  90
      919
      920   GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC   527
      921   Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
      922                       95                  100                 105
      923
      924   CGA AAG GAA ATC GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC   572
      925   Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
      926                       110                 115                 120
      927
      928   CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT   617
      929   Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
      930                       125                 130                 135
      931
      932   TGG AGT GAA AAC CTTTTC CAG TGC TTC AAT TGC AGC CTC TGC CTC   662
      933   Trp Ser Glu Asn LeuPhe Gln Cys Phe Asn Cys Ser Leu Cys Leu
      934                       140             145             150
      935
      936   AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG   707
      937   Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
```

spaces are shown in submitted file - if this represents a gap the sequence, separate sequences must be shown (see 1.822(o) of Sequence Rules for explanation)

```
938                         155                    160                    165
939
940   TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC   752
941   Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
942                         170                    175                    180

943
944   TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC AGG AAG TTG TGC   797
945   Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
946                         185                    190                    195

947
948   CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC   842
949   Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
950                         200                    205                    210

951
952   ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA   887
953   Thr Val Leu Leu ProLeu Val Ile Phe Phe Gly Leu Cys Leu Leu
954                         215 [gap?]              220                    225

955
956   TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG   932
957   Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
958                         230                    235                    240

959
960   TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA   977
961   Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
962                         245                    250                    255

963
964   GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC   1022
965   Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
966                         260                    265                    270

967
968   CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC   1067
969   Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
970                         275                    280                    285

971
972   AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC   1112
973   Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
974                         290                    295                    300

975
976   CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA   1157
977   Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
978                         305                    310                    315

979
980   CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC   1202
981   Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
982                         320                    325                    330

983
984   TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC   1247
985   Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala
986                         335                    340                    345

987
988   CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC   1292
989   His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
990                         350                    355                    360
```

```
991
992    GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAGGAATTC        1334
993    Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
994                    365                 370
995
996
```

```
 997    (2) INFORMATION FOR SEQ ID NO:66:
 998
 999    (i) SEQUENCE CHARACTERISTICS:
1000    (A) LENGTH:371 amino acids
1001    (B) TYPE:polypeptide
1002
1003    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1004
1005    Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
1006                     5                 10                 15
1007    Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
1008                    20                 25                 30
1009    Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
1010                    35                 40                 45
1011    Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
1012                    50                 55                 60
1013    Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
1014                    65                 70                 75
1015    Gly Gln Asp The Asp Cys Arg Glu Cys Gly Ser Gly Ser Phe Thr
1016                    80                 85                 90
1017    Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
1018                    95                100                105
1019    Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
1020                   110                115                120
1021    Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
1022                   125                130                135
1023    Trp Ser Glu Asn LeuPhe Gln Cys Phe Asn Cys Ser Leu Cys Leu
1024                   140                145                150
1025    Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
1026                   155                160                165
1027    Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
1028                   170                175                180
1029    Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
1030                   185                190                195
1031    Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
1032                   200                205                210
1033    Thr Val Leu Leu ProLeu Val Ile Phe Phe Gly Leu Cys Leu Leu
1034                   215                220                225
1035    Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
1036                   230                235                240
1037    Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
1038                   245                250                255
1039    Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
1040                   260                265                270
1041    Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
1042                   275                280                285
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/383,676*

INPUT SET: S31123.raw

```
1043   Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1044                   290             295             300
1045   Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
1046                   305             310             315
1047   Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
1048                   320             325             330
1049   Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala
1050                   335             340             345
1051   His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
1052                   350             355             360
1053   Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
1054                   365             370
1055
```

```
1056   (2)  INFORMATION FOR SEQ ID NO:67:
1057
1058   (i)  SEQUENCE CHARACTERISTICS:
-->  1059   (A) LENGTH:6464 bases
1060   (B) TYPE:nucleic acid
1061   (C) STRANDEDNESS:single
1062   (D) TOPOLOGY:linear
1063
1064   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
1065
1066   TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT    50
1067   TAGTTCATAG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT   100  GGCCCGCCTC GCTGACCGCC  C
1068   CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTIGGCAGT   350  ACATCTACGT ATTAGTCATC  G
1069   AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACTATAGG   650  GAGACCCAAG CTTCTGCAGG  T
1070   AGGTTTTACT TGCTTTAAAA AACCTCCCAC ACCTCCCCCT GAACCTGAAA  1250  CATAAAATGA ATGCAATTGT  T
1071   GTTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATTC ACGTAAACAG  1550  AAGATTCCGC CTCAAGTTCC  G
1072   CCCACCACCT GGCCCCGCCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC  1850  GCAGCCAAGG CGGACGGGTA  G
1073   GCGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC  2150  CTCGTGGAGG CGGGGCCTCT  G
1074   TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG  2450  CACTTGGCGG AGACGCGCGG  G
1075   GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAG  2750  GTAAACAGAA CCTGGTGATT  A
1076   AGGCCATCTC AGACTCTTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG  3050  ACACGTTCTT CCCAGAAATT  G
1077   GCAGAGCTAG AACTCAGACT TTAAAGAAAA TTAGATCAAA GTAGAGACTG  3650  AATTATTCTG CACATCAGAC  T
1078   ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC CAGGCTCCCC  4000  AGCAGGCAGA AGTATGCAAA  G
1079   CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA  4255  CCGCTACACT TGCCAGCGCC  C
1080   GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG TTTTTGCTCA  4850  CCCAGAAACG CTGGTGAAAG  T
1081   GAAAAGCATC TTACGGATGG CATGACAGTA AGAGKATTAT GCAGTGCTGC  5150  CATAACCATG AGTGATAACA  C
1082   TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC  5450  GGCTGGCTGG TTTATTGCTG  A
1083   AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA CCAAAATCCC  5750  TTAACGTGAG TTTTCGTTCC  A
1084   GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC  6100  TGCCAGTGGC GATAAGTCGT  G
1085   GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT  6400  TGAGCGTCGA TTTTTGTGAT  G
1086
```

```
1087   (2)  INFORMATION FOR SEQ ID NO:68:
1088
1089   (i)  SEQUENCE CHARACTERISTICS:
-->  1090   (A) LENGTH:2173 bases
1091   (B) TYPE:nucleic acid
1092   (C) STRANDEDNESS:single
1093   (D) TOPOLOGY:linear
```

INPUT SET: S31123.raw

1094
1095   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
1096
1097   GAATTCCTTT TCTCCGAGTT TTCTGAACTC TGGCTCATGA TCGGGCTTAC   50 TGGATACGAG AATCCTG
1098

--> 1099   ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC   289
     1100   Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
     1101   5   10   15
     1102
     1103   CTG GCT CTG CTG ATG GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG   334
     1104   Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu
     1105   20   25   30
     1106
     1107   GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG GAT AAT TTG TGT CCC   379
     1108   Val Pro Ser Leu Gly Asp Ara Glu Lys Arg Asp Asn Leu Cys Pro
     1109   35   40   45
     1110
     1111   CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC   424
     1112   Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cvs Thr
     1113   50   55   60
     1114
     1115   AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA   469
     1116   Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
     1117   65   70   75
     1118
     1119   GGG CAG GAA ACA GTC TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA   514
     1120   Gly Gln Glu Thr Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr
     1121   80   85   90
     1122
     1123   GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC AGT TGC AAG ACA TGT   559
     1124   Ala Ser Gln Asn His Val Arg Gln Cys Leu Ser Cys Lys Thr Cys
     1125   95   100   105
     1126
     1127   CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC   604
     1128   Arg Lys Glu Yet Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp
     1129   110   115   120
     1130
--> 1131   ATG GAC ACC GTG TGT GGC TGC AAG GAG AAC CAA TTC CAG CGC TAC   649
     1132   Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr
     1133   125   130   135
     1134
     1135   CTG AGT GAG ACG CAT TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC   694
     1136   Leu Ser Glu Thr His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe
     1137   140   145   150
     1138
     1139   AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG AAA CAG AAC ACC GTG   739
     1140   Asn Gly Thr Val Thr Ile Pro Cys Lys Glu Lys Gln Asn Thr Val
     1141   155   160   165
     1142
     1143   TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC   784
     1144   Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr
     1145   170   175   180
     1146

```
1147    CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC  829
1148    Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys
1149                185               190               195
1150

1151    CTA CCT CCA GTT GCA AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT  874
1152    Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser Gly Thr
1153                200               205               210
1154
```

invalid for use in the sequence-use "N" and explain in (ix) FEATURE: section (handwritten annotation)

```
-->  1155   GCC GTC CTG TTG CCT CTG GTT ATC TTC CTA GGT CTT TGC CTT TTA  919
1156    Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu Leu
1157                215               220               225
1158

1159    TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG  964
1160    Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg
1161                230               235               240
1162

1163    CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA 1009
1164    Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys
1165                245               250               255
1166

1167    GAG GTG GAG GGT GAA GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC 1054
1168    Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala
1169                260               265               270
1170

1171    TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC TTC AAC CCC ACT CTG 1099
1172    Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu
1173                275               280               285
1174

1175    GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC 1144
1176    Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr
1177                290               295               300
1178

1179    CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG 1189
1180    Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val
1181                305               310               315
1182

1183    CCA CCT GTA AGA GAG GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC 1234
1184    Pro Pro Val Arg Glu Val Val Pro Thr Gln Gly Ala Asp Pro Leu
1185                320               325               330
1186

1187    CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC CCC GCC CCT GTT CGG 1279
1188    Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile Pro Ala Pro Val Arg
1189                335               340               345
1190

1191    AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT 1324
1192    Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
1193                350               355               360
1194

1195    GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG 1369
1196    Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro
1197                365               370               375
1198

1199    ACA CGC TGG AAG GAG TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC 1414
```

INPUT SET: S31123.raw

```
1200    Thr Arg Trp Lys Glu Phe Met Arg Leu Leu Gly Leu Ser Glu His
1201                380             385         390
1202
1203    GAG ATC GAG CGG TTG GAG CTG CAG AAC GGG CGT TGC CTC CGC GAG 1459
1204    Glu Ile Glu Arc Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu
1205                395             400         405
1206
1207    GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA 1504
1208    Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
1209                410             415         420
1210
1211    CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG 1549
1212    His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met
1213                425             430         435
1214
1215    AAC CTG CGT GGC TGC CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC 1594
1216    Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser
1217                440             445         450
1218
1219    CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG CGA TAAGGCCACA       1637
1220    Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
1221                455             460
1222
1223    CCCCCACCTC AGGAACGGGA CTCGAAGGAC CATCCTGCTA GATGCCCTGC   1687 TTCCCTGTGA ACCTCCT
1224    GGGAAGTGTG CCATCTGCTC CCAGACAGCT GAGGGTGCCA AAAGCCAGGA   1887
1225    GAGGTGATTG TGGAGAAAAA GCACAATCTA TCTGATACCC ACTTGGGATG   1937
1226    CAAGGACCCA AACAAAGCTT CTCAGGGCCT CCTCAGTTGA TTTCTGGGCC   1987
1227    CTTTTCACAG TAGATAAAAC AGTCTTTGTA TTGATTATAT CACACTAATG   2037
1228    GATGAACGGT TGAACTCCCT AAGGTAGGGG CAAGCACAGA ACAGTGGGGT   2087
1229    CTCCAGCTGG AGCCCCCGAC TCTTGTAAAT ACACTAAAAA TCTAAAAGTG   2137
1230    AAAAAAAAAA AAAAAAAAAA AAAAAAAAAG GAATTC               2173
1231
```
--> 1224 (row emphasized)

```
1232    (2) INFORMATION FOR SEQ ID NO:69:
1233
1234    (i) SEQUENCE CHARACTERISTICS:
```
--> 1235   (A) LENGTH:461 amino acids
--> 1236   (B) TYPE:polypeptide
```
1237
```
--> 1238   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
```
1239
1240    Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
1241                5             10              15
1242    Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu
1243                20            25              30
1244    Val Pro Ser Leu Gly Asp Ara Glu Lys Arg Asp Asn Leu Cys Pro
1245                35            40              45
1246
1247    Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cvs Thr
1248                50            55              60
1249    Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
1250                65            70              75
1251    Gly Gln Glu Thr Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr
```

INPUT SET: S31123.raw

```
1252                          80                    85                    90
1253    Ala Ser Gln Asn His Val Arg Gln Cys Leu Ser Cys Lys Thr Cys
1254                          95                   100                   105
1255    Arg Lys Glu Yet Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp
1256                         110                   115                   120
1257    Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr
1258                         125                   130                   135
1259    Leu Ser Glu Thr His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe
1260                         140                   145                   150
1261    Asn Gly Thr Val Thr Ile Pro Cys Lys Glu Lys Gln Asn Thr Val
1262                         155                   160                   165
1263    Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr
1264                         170                   175                   180
1265    Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys
1266                         185                   190                   195
1267    Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser Gly Thr
1268                         200                   205                   210
1269    Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu Leu
1270                         215                   220                   225
1271    Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg
1272                         230                   235                   240
1273    Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys
1274                         245                   250                   255
1275    Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala
1276                         260                   265                   270
1277    Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu
1278                         275                   280                   285
1279    Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr
1280                         290                   295                   300
1281    Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val
1282                         305                   310                   315
1283    Pro Pro Val Arg Glu Val Val Pro Thr Gln Gly Ala Asp Pro Leu
1284                         320                   325                   330
1285    Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile Pro Ala Pro Val Arg
1286                         335                   340                   345
1287    Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
1288                         350                   355                   360
1289    Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro
1290                         365                   370                   375
1291    Thr Arg Trp Lys Glu Phe Met Arg Leu Leu Gly Leu Ser Glu His
1292                         380                   385                   390
1293    Glu Ile Glu Arc Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu
1294                         395                   400                   405
1295    Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
1296                         410                   415                   420
1297    His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met
1298                         425                   430                   435
1299    Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser
1300                         440                   445                   450
1301    Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
1302                         455                   460
1303
```

```
1412    (2) INFORMATION FOR SEQ ID NO:71:
```

INPUT SET: S31123.raw

```
1413
1414   (i)  SEQUENCE CHARACTERISTICS:
-->  1415   (A)  LENGTH:340 amino acids
-->  1416   (B)  TYPE:polypeptide
1417
-->  1418   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
1419
1420   Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
1421                    5                  10                  15
1422   Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
1423                   20                  25                  30
1424   Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
1425                   35                  40                  45
1426
1427   Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
1428                   50                  55                  60
1429   Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
1430                   65                  70                  75
1431   Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
1432                   80                  85                  90
1433   Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
1434                   95                 100                 105
1435   Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
1436                  110                 115                 120
1437   Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
1438                  125                 130                 135
1439   Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
1440                  140                 145                 150
1441   Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
1442                  155                 160                 165
1443   Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
1444                  170                 175                 180
1445   Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
1446                  185                 190                 195
1447   Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
1448                  200                 205                 210
1449   Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
1450                  215                 220                 225
1451   Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
1452                  230                 235                 240
1453   Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
1454                  245                 250                 255
1455   Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
1456                  260                 265                 270
1457   Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
1458                  275                 280                 285
1459   Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1460                  290                 295                 300
1461   Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
1462                  305                 310                 315
1463   Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
1464                  320                 325                 330
1465   Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys
```

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/383,676*

INPUT SET: S31123.raw

```
1466                    335                    340
1467
1468
```

```
1469   (2)  INFORMATION FOR SEQ ID NO:72:
1470
1471   (i)  SEQUENCE CHARACTERISTICS:
1472   (A)  LENGTH:19 bases
1473   (B)  TYPE:nucleic acid
1474   (C)  STRANDEDNESS:single
1475   (D)  TOPOLOGY:linear
1476
1477   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:72:
1478
1479   GTACTTGAAC TCGTTCCTG                          19
1480
1481
1482
1483
1484
1485
1486
1487
```

last sequence in file

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/383,676*

INPUT SET: S31123.raw

Line	Error	Original Text
9	Number of Sequences (64) Doesn't Equal Actual Count (71)	(iii) NUMBER OF SEQUENCES:64
26	Wrong application Serial Number	(A) APPLICATION NUMBER:08/484,312
42	Entered (1365) and Calc. Seq. Length (0) differ	(A) LENGTH:1365 bases
54	Entered (483) and Calc. Seq. Length (0) differ	(A) LENGTH:483 bases
66	Entered (455) and Calc. Seq. Length (0) differ	(A) LENGTH:455 amino acids
67	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
69	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
69	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
137	Entered (161) and Calc. Seq. Length (0) differ	(A) LENGTH:161 amino acids
138	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
140	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
140	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
168	Entered (157) and Calc. Seq. Length (0) differ	(A) LENGTH:157 bases
180	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
181	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
183	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
183	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
191	Entered (11) and Calc. Seq. Length (0) differ	(A) LENGTH:11 amino acids
192	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
194	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
194	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
202	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH:12 amino acids
203	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
205	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
205	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
213	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
214	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
216	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
216	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
224	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
225	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
227	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
227	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
227	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
232	Sequence * missing	(12) INFORMATION FOR SEQ ID NO:11:
235	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH:15 amino acids
236	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
238	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
246	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
247	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
249	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
249	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
257	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
258	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
260	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
260	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
268	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH:20 amino acids

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/383,676*

INPUT SET: S31123.raw

Line	Error	Original Text
269	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
271	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
271	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
281	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH:19 amino acids
282	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
284	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
284	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
294	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH:18 amino acids
295	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
297	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
297	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
307	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
308	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
310	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
310	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
318	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
319	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
321	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
321	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
329	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
330	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
332	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
332	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
484	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
485	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
487	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
487	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
495	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
496	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
498	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
498	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
650	Entered (51) and Calc. Seq. Length (0) differ	(A) LENGTH:51 amino acids
651	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
653	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
653	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
667	Entered (158) and Calc. Seq. Length (0) differ	(A) LENGTH:158 bases
765	Entered (63) and Calc. Seq. Length (0) differ	(A) LENGTH:63 bases
777	Entered (64) and Calc. Seq. Length (0) differ	(A) LENGTH:64 bases
813	Entered (81) and Calc. Seq. Length (0) differ	(A) LENGTH:81 bases
873	Entered (30) and Calc. Seq. Length (18) differ	(A) LENGTH:30 bases
885	Entered (1334) and Calc. Seq. Length (1134) differ	(A) LENGTH:1334 bases
894	# of Sequences for line conflicts w/ running total	TAGCTGTCTG GC
1000	Entered (371) and Calc. Seq. Length (0) differ	(A) LENGTH:371 amino acids
1001	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1003	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1003	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1059	Entered (6464) and Calc. Seq. Length (50) differ	(A) LENGTH:6464 bases
1090	Entered (2173) and Calc. Seq. Length (1727) differ	(A) LENGTH:2173 bases

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/383,676*

INPUT SET: S31123.raw

Line	Error	Original Text
1099	# of Sequences for line conflicts w/ running total	ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CT
1131	Wrong Nucleic Acid Designator	ATG GAC ACC GTG TGT GGC TGC AAG PAG AkC CA
1131	# of Sequences for line conflicts w/ running total	ATG GAC ACC GTG TGT GGC TGC AAG PAG AkC CA
1155	Wrong Nucleic Acid Designator	GCC GIC CTG TTG CCT CTG GTT ATC TTC CTA GGT
1155	# of Sequences for line conflicts w/ running total	GCC GIC CTG TTG CCT CTG GTT ATC TTC CTA GGT
1224	# of Sequences for line conflicts w/ running total	GGGAAGTGTG CCATCTGCTC CCAGACAGCT GAGGG
1235	Entered (461) and Calc. Seq. Length (0) differ	(A) LENGTH:461 amino acids
1236	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1238	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1415	Entered (340) and Calc. Seq. Length (0) differ	(A) LENGTH:340 amino acids
1416	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1418	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
1418	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: